



(1) GENERAL INFORMATION:

- (i) APPLICANT: Price, David H.
- (ii) TITLE OF INVENTION: P-TEFb COMPOSITIONS, METHODS AND SCREENING ASSAYS
- (iii) NUMBER OF SEQUENCES: 68
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Williams, Morgan & Amerson, P.C.
 - (B) STREET: 10333 Richmond, #1100
 - (C) CITY: Houston
 - (D) STATE: TX
 - (E) COUNTRY: USA
 - (F) ZIP: 77042
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/951,188
 - (B) FILING DATE: 1997-10-15
 - (C) CLASSIFICATION: Unknown
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Fussey, Shelley P.M.
 - (B) REGISTRATION NUMBER: 39,458
 - (C) REFERENCE/DOCKET NUMBER: 4200.000200
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (713) 934-7000
 - (B) TELEFAX: (713) 934-7011

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 115..1326
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGTTGAGTCA ACAGCTGTAG ATACACCAAT TGTTGCCGAT TTCTTTCTTT TCGACTGTCTG	60
GCTTCTCGCG AAAGTGTGAT TGTGAAAATT GTACAAATAG AGGCAAATTT AACC ATG	117
Met	
1	

GCG CAC ATG TCC CAC ATG CTC CAG CAG CCT TCG GGG TCG ACG CCC TCC	165
Ala His Met Ser His Met Leu Gln Gln Pro Ser Gly Ser Thr Pro Ser	
5 10 15	
AAC GTG GGC TCC AGC TCA TCG CGC ACG ATG TCC CTG ATG GAG AAA CAA	213
Asn Val Gly Ser Ser Ser Ser Arg Thr Met Ser Leu Met Glu Lys Gln	
20 25 30	
AAG TAC ATC GAG GAC TAC GAC TTT CCC TAC TGC GAC GAG AGC AAC AAA	261
Lys Tyr Ile Glu Asp Tyr Asp Phe Pro Tyr Cys Asp Glu Ser Asn Lys	
35 40 45	
TAC GAA AAG GTG GCG AAA ATT GGC CAA GGC ACC TTC GGA GAG GTT TTT	309
Tyr Glu Lys Val Ala Lys Ile Gly Gln Gly Thr Phe Gly Glu Val Phe	
50 55 60 65	
AAG GCT CGC GAG AAA AAG GGC AAC AAG AAG TTT GTG GCC ATG AAG AAG	357
Lys Ala Arg Glu Lys Lys Gly Asn Lys Lys Phe Val Ala Met Lys Lys	
70 75 80	
GTG CTG ATG GAC AAC GAA AAG GAG GGC TTT CCC ATC ACG GCT CTG CGA	405
Val Leu Met Asp Asn Glu Lys Glu Gly Phe Pro Ile Thr Ala Leu Arg	
85 90 95	
GAG ATC CGC ATC CTG CAG CTG CTA AAG CAC GAG AAC GTG GTG AAT CTG	453
Glu Ile Arg Ile Leu Gln Leu Leu Lys His Glu Asn Val Val Asn Leu	
100 105 110	
ATC GAG ATC TGC CGC ACC AAG GCC ACC GCC ACG AAT GGT TAC AGA TCC	501
Ile Glu Ile Cys Arg Thr Lys Ala Thr Ala Thr Asn Gly Tyr Arg Ser	
115 120 125	
ACC TTC TAT TTG GTC TTT GAT TTC TGC GAA CAC GAT TTG GCA GGT CTT	549
Thr Phe Tyr Leu Val Phe Asp Phe Cys Glu His Asp Leu Ala Gly Leu	
130 135 140 145	
CTG TCC AAC ATG AAC GTC AAG TTC AGT CTG GGC GAG ATT AAG AAG GTT	597
Leu Ser Asn Met Asn Val Lys Phe Ser Leu Gly Glu Ile Lys Lys Val	
150 155 160	
ATG CAG CAG CTT TTA AAC GGT TTG TAT TAC ATC CAC AGC AAC AAG ATC	645
Met Gln Gln Leu Leu Asn Gly Leu Tyr Tyr Ile His Ser Asn Lys Ile	
165 170 175	
CTG CAC CGA GAC ATG AAA GCT GCC AAC GTG CTG ATT ACC AAG CAT GGC	693
Leu His Arg Asp Met Lys Ala Ala Asn Val Leu Ile Thr Lys His Gly	
180 185 190	
ATC TTA AAG CTG GCT GAC TTT GGC TTG GCC CGT GCT TTT AGC ATT CCA	741
Ile Leu Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Ser Ile Pro	
195 200 205	
AAG AAC GAG AGT AAG AAT CGC TAT ACC AAT CGC GTA GTA ACC TTG TGG	789
Lys Asn Glu Ser Lys Asn Arg Tyr Thr Asn Arg Val Val Thr Leu Trp	
210 215 220 225	

TAC CGG CCG CCT GAG CTG CTA CTT GGT GAC CGC AAC TAT GGT CCA CCC Tyr Arg Pro Pro Glu Leu Leu Leu Gly Asp Arg Asn Tyr Gly Pro Pro 230 235 240	837
GTG GAC ATG TGG GGA GCC GGC TGC ATA ATG GCC GAG ATG TGG ACA CGC Val Asp Met Trp Gly Ala Gly Cys Ile Met Ala Glu Met Trp Thr Arg 245 250 255	885
TCG CCC ATC ATG CAA GGC AAT ACG GAG CAG CAG CAG TTA ACC TTT ATT Ser Pro Ile Met Gln Gly Asn Thr Glu Gln Gln Gln Leu Thr Phe Ile 260 265 270	933
TCG CAG CTA TGC GGC TCC TTT ACG CCG GAC GTG TGG CCG GGA GTG GAG Ser Gln Leu Cys Gly Ser Phe Thr Pro Asp Val Trp Pro Gly Val Glu 275 280 285	981
GAG CTG GAG CTG TAC AAA TCC ATC GAG CTG CCA AAG AAC CAG AAG CGT Glu Leu Glu Leu Tyr Lys Ser Ile Glu Leu Pro Lys Asn Gln Lys Arg 290 295 300 305	1029
CGA GTC AAG GAG CGC CTG CGT CCG TAT GTC AAG GAT CAA ACC GGC TGT Arg Val Lys Glu Arg Leu Arg Pro Tyr Val Lys Asp Gln Thr Gly Cys 310 315 320	1077
GAT CTA TTG GAC AAA TTG CTG ACC CTT GAT CCC AAG AAA CGC ATC GAT Asp Leu Leu Asp Lys Leu Leu Thr Leu Asp Pro Lys Lys Arg Ile Asp 325 330 335	1125
GCG GAC ACA GCT CTG AAT CAC GAC TTC TTC TGG ACG GAT CCC ATG CCC Ala Asp Thr Ala Leu Asn His Asp Phe Phe Trp Thr Asp Pro Met Pro 340 345 350	1173
AGC GAC TTG AGC AAG ATG CTG TCC CAG CAC CTG CAG AGC ATG TTC GAG Ser Asp Leu Ser Lys Met Leu Ser Gln His Leu Gln Ser Met Phe Glu 355 360 365	1221
TAC CTG GCG CAG CCA CGC CGC AGC AAC CAG ATG CGC AAC TAT CAC CAG Tyr Leu Ala Gln Pro Arg Ser Asn Gln Met Arg Asn Tyr His Gln 370 375 380 385	1269
CAA CTG ACC ACC ATG AAC CAG AAG CCC CAG GAC AAC AGT ATG ATT GAC Gln Leu Thr Thr Met Asn Gln Lys Pro Gln Asp Asn Ser Met Ile Asp 390 395 400	1317
CGG GTT TGG TAGACTGCCA GAGGTGTACG CACCCGACTA ATAGTTTCTC Arg Val Trp	1366
ACCTTCAACT AGCGTTAGGT TATTAGGTTA GTGTACAATA AAAATATTGG CATTGTCATT	1426
AGCGCTTGCT CCAAATATAA AAAAAAAAAA A	1457

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	His	Met	Ser	His	Met	Leu	Gln	Gln	Pro	Ser	Gly	Ser	Thr	Pro	
1				5					10					15		
Ser	Asn	Val	Gly	Ser	Ser	Ser	Ser	Arg	Thr	Met	Ser	Leu	Met	Glu	Lys	
			20					25					30			
Gln	Lys	Tyr	Ile	Glu	Asp	Tyr	Asp	Phe	Pro	Tyr	Cys	Asp	Glu	Ser	Asn	
		35					40					45				
Lys	Tyr	Glu	Lys	Val	Ala	Lys	Ile	Gly	Gln	Gly	Thr	Phe	Gly	Glu	Val	
	50					55					60					
Phe	Lys	Ala	Arg	Glu	Lys	Lys	Gly	Asn	Lys	Lys	Phe	Val	Ala	Met	Lys	
65					70					75					80	
Lys	Val	Leu	Met	Asp	Asn	Glu	Lys	Glu	Gly	Phe	Pro	Ile	Thr	Ala	Leu	
				85					90						95	
Arg	Glu	Ile	Arg	Ile	Leu	Gln	Leu	Leu	Lys	His	Glu	Asn	Val	Val	Asn	
			100					105					110			
Leu	Ile	Glu	Ile	Cys	Arg	Thr	Lys	Ala	Thr	Ala	Thr	Asn	Gly	Tyr	Arg	
	115						120					125				
Ser	Thr	Phe	Tyr	Leu	Val	Phe	Asp	Phe	Cys	Glu	His	Asp	Leu	Ala	Gly	
	130					135					140					
Leu	Leu	Ser	Asn	Met	Asn	Val	Lys	Phe	Ser	Leu	Gly	Glu	Ile	Lys	Lys	
145				150						155					160	
Val	Met	Gln	Gln	Leu	Leu	Asn	Gly	Leu	Tyr	Tyr	Ile	His	Ser	Asn	Lys	
			165						170					175		
Ile	Leu	His	Arg	Asp	Met	Lys	Ala	Ala	Asn	Val	Leu	Ile	Thr	Lys	His	
		180					185						190			
Gly	Ile	Leu	Lys	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Phe	Ser	Ile	
	195					200					205					
Pro	Lys	Asn	Glu	Ser	Lys	Asn	Arg	Tyr	Thr	Asn	Arg	Val	Val	Thr	Leu	
	210					215					220					
Trp	Tyr	Arg	Pro	Pro	Glu	Leu	Leu	Leu	Gly	Asp	Arg	Asn	Tyr	Gly	Pro	
225				230					235						240	
Pro	Val	Asp	Met	Trp	Gly	Ala	Gly	Cys	Ile	Met	Ala	Glu	Met	Trp	Thr	
			245					250						255		
Arg	Ser	Pro	Ile	Met	Gln	Gly	Asn	Thr	Glu	Gln	Gln	Gln	Leu	Thr	Phe	

260	265	270
Ile Ser Gln Leu Cys Gly Ser Phe Thr Pro Asp Val Trp Pro Gly Val		
275	280	285
Glu Glu Leu Glu Leu Tyr Lys Ser Ile Glu Leu Pro Lys Asn Gln Lys		
290	295	300
Arg Arg Val Lys Glu Arg Leu Arg Pro Tyr Val Lys Asp Gln Thr Gly		
305	310	315
Cys Asp Leu Leu Asp Lys Leu Leu Thr Leu Asp Pro Lys Lys Arg Ile		
325	330	335
Asp Ala Asp Thr Ala Leu Asn His Asp Phe Phe Trp Thr Asp Pro Met		
340	345	350
Pro Ser Asp Leu Ser Lys Met Leu Ser Gln His Leu Gln Ser Met Phe		
355	360	365
Glu Tyr Leu Ala Gln Pro Arg Arg Ser Asn Gln Met Arg Asn Tyr His		
370	375	380
Gln Gln Leu Thr Thr Met Asn Gln Lys Pro Gln Asp Asn Ser Met Ile		
385	390	395
		400
Asp Arg Val Trp		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAGCCCTGCC GACGGCCATA CTTGAAAATA CATTTTTTTC TGCAAAGTTT GTCATTGTCA	60
CTGTGTGAAT GGAATCTGTG ATGTGTTGTG GAATTAAAAA CGTCAAGTAA ACAACCCGTA	120
ATGGTTAAAG TGCACGGCGA AAGCAGTGCG AATAACTATG AATTGATACA AAAGTTGCAT	180
AACACGTCGC CTGGTGTGCG GGTAGTGTG TTTTTCGTCT CGTTTCGTTT CCGCCGCAGT	240
CGCAGTTTCC AAAAAACCTC ACCACACCAT ACCATCTCCA CCACGCACAC ACACACACAA	300
ACAAACACGC AGAGACGCGG CGGCGGAAAA AGTGTGCGGA CCGCGGATTT AACCCCTCGT	360
TCCAAACCCA AATTGGAGTC TCCCAAAAAC AGCGAAATAT CGAGTGTGGC TTAGCCGATG	420
TGCCGTGCGA TCCCCACTGC CCCTTCCGTA CCGCTGCCAC CCCC GCCACA GCAGCAACGC	480
ACACGGATAC GGACACAGAC ACCAATACCA GCGCACTCAA GCACGGCCGA CAAAGAAAGA	540

GCGCTCTCCC	TTCCTCTTTG	TACAGTTAGT	TCCTACAGCT	GAATCAGCCA	AAAGAAATTA	600
CTAGGTCCAT	TCCGAGGCGC	AGTTTGCATG	TGAAACGGAG	GTCCCCGCAT	AACCACGCGG	660
AACCCGAAAT	TCCAGATCCC	CATCTCCGCT	GCACGGATAA	AGGAAACATA	CAACCATGAG	720
TCTCCTAGCC	ACGCCAATGC	CCCAGGCGGC	CACCGCCTCA	TCTTCTTCAT	CCGCCTCCGC	780
GGCCGCCTCG	GCCAGCGGGA	TTCCAATCAC	CGCCAACAAC	AACCTGCCTT	TCGAGAAGGA	840
CAAGATCTGG	TACTTCAGCA	ACGATCAGCT	GGCCAATTTG	CCAAGCAGAA	GATGCGGCAT	900
CAAGGGCGAC	GATGAGCTGC	AGTACCGCCA	GATGACCGCC	TATCTGATAC	AGGAAATGGG	960
TCAGCGTCTG	CAGGTGTCCC	AACTGTGCAT	CAACACGGCC	ATTGTGTACA	TGCATCGGTT	1020
CTACGCCTTT	CACTCCTTCA	CCCACTTTCA	TCGCAACTCC	ATGGCGTCGG	CGAGCCTCTT	1080
CTTGCGCGCC	AAGGTAGAAG	AGCAACCGCG	GAAGCTGGAG	CATGTTATTC	GGGCGCCAA	1140
CAAGTGCCTG	CCGCCGACCA	CCGAGCAGAA	TTACGCCGAA	CTCGCCCAGG	AGCTTGTGTT	1200
CAACGAGAAC	GTGCTCCTGC	AGACGCTGGG	CTTCGATGTG	GCCATCGATC	ATCCGCACAC	1260
GCATGTGGTG	CGCACCTGCC	AGCTGGTCAA	AGCATGCAAG	GATCTGGCGC	AGACATCGTA	1320
CTTCTTGGCC	TCGAACAGCC	TGCATCTGAC	CTCGATGTGC	CTCCAATATC	GCCCCACGGT	1380
CGTAGCCTGT	TTCTGCATTT	ACCTAGCCTG	CAAGTGGTCC	CGATGGGAGA	TCCCCAGTC	1440
GACCGAGGGC	AAGCACTGGT	TCTACTATGT	GGACAAGACG	GTCTCGCTGG	ATTTGCTAAA	1500
GCAGCTGACA	GATGAGTTCA	TCGCTATCTA	TGAGAAGAGC	CCGGCCCCGC	TGAAGTCTAA	1560
GCTTAACTCG	ATCAAGGCGA	TCGCCCAGGG	AGCCAGCAAT	CGGACAGCTA	ACAGCAAGGA	1620
CAAACCAAAG	GAGGACTGGA	AGATCACCGA	GATGATGAAG	GGCTACCACT	CAAACATCAC	1680
GACACCACCA	GAGCTGTTAA	ACGGCAACGA	CAGCCGGGAT	CGGGACCGAG	ATCGTGAACG	1740
GGAGAGAGAG	CGGGAACGGG	ATCCGTCGTC	ACTACTGCCG	CCACCGGCTA	TGGTGCCGCA	1800
GCAAAGACGA	CAGGATGGTG	GACATCAGCG	CTCGTCCTCA	GTGAGCGGAG	TGCCAGGCAG	1860
CAGCTCTTCG	TCGTCTTCCT	CCAGTCACAA	GATGCCAAAT	TACCCTGGTG	GCATGCCGCC	1920
CGAAGCTCAT	CCGGATCACA	AGTCAAAGCA	GCCGGGCTAT	AACAATCGAA	TGCCCTCAAG	1980
TCACCAGCGT	AGTAGTAGCA	GTGGACTCGG	TTCCTCGGGA	AGTGGCAGCC	AGCACAGCAG	2040
CTCATCCTCG	TCGTCTTCAA	GCCAGCAGCC	TGGCCGACCG	TCTATGCCCG	TGGACTATCA	2100
CAAATCCTCT	CGCGGCATGC	CGCCGGTAGG	CGTGGGCATG	CCACCTCACG	GCAGCCACAA	2160
GATGACTTCG	GGCTCCAAGC	CTCAACAGCC	GCAGCAGCAG	CCGGTCCCAC	ATCCATCCGC	2220

CTCTAATTCC	TCTGCATCGG	GCATGTCCTC	CAAGGATAAA	TCCCAGAGCA	ACAAAATGTA	2280
TCCGAACGCA	CCGCCGCCAT	ACAGTAATAG	TGCCCCCTCA	AACCCGCTGA	TGTCGCGTGG	2340
TGGATATCCA	GGCGCTAGCA	ATGGATCCCA	GCCCCCGCCT	CCCGCCGGAT	ACGGCGGCCA	2400
TCGCAGCAAA	TCCGGCTCCA	CCGTCCATGG	CATGCCGCAT	TTCGAGCAGC	AATTGCCCTA	2460
TCCCAGAGC	CAGAGCTACG	GCCACATGCA	GCAGCAGCCA	GTGCCTCAGT	CTCAGCAGCA	2520
ACAGATGCCT	CCGGAGGCAT	CCCAGCACTC	GTTGCAGTCC	AAGAACTCGC	TCTTCAGTCC	2580
AGAGTGGCCA	GACATTAAAA	AGGAGCCCAT	GTCGCAGTCG	CAACCACAGC	TTTTTAACGG	2640
TTTGCTACCC	CCTCCTGCGC	CTCCCGGCCA	CGATTACAAG	CTAAATAGCC	ATCCGCGCGA	2700
CAAAGAAAGT	CCCAAGAAAG	AGCGACTAAC	GCCAACCAAA	AAGGATAAGC	ACCGTCCTGT	2760
AATGCCCCCA	ATGGGCAGTG	GGAACAGTTC	CTCCGGCTCG	GGATCATCAA	AGCCGATGCT	2820
ACCGCCTCAC	AAGAAGCAGA	TACCCCATGG	CGGGGACCTG	TTGACCAATC	CTGGAGAGAG	2880
TGGAAGCCTA	AAACGGCCCA	ACGAGATCTC	GGGAAGTCAG	TATGGACTAA	ATAAGCTGGA	2940
TGAAATAGAT	AACAGTAATA	TGCCTCGAGA	AAAGCTTCGC	AAGCTGGACA	CTACAACCTG	3000
ACTACCAACT	TATCCGAATT	ATGAGGAGAA	ACACACGCCT	CTGAATATGT	CCAACGGAAT	3060
CGAGACAACG	CCGGATCTGG	TGCGCAGTTT	GCTAAAGGAG	AGTCTGTGTC	CATCGAACGC	3120
TTCGCTCCTG	AAACCGGATG	CCTTGACTAT	GCCTGGCCTG	AAACCACCGG	CCGAACACT	3180
TGAGCCCATG	CCCGCACCAG	CGACAATCAA	GAAAGAACAG	GGAATAACTC	CGATGACCAG	3240
TTTGGCTAGT	GGGCCC GCAC	CCATGGATTT	GGAAGTACCC	ACTAAACAGG	CCGGAGAGAT	3300
TAAGGAGGAA	AGCAGCAGCA	AGTCCGAAAA	GAAAAAGAAG	AAGGATAAAC	ACAAACACAA	3360
GGAGAAGGAC	AAGTCCAAGG	ACAAGACGGA	AAAGGAGGAG	CGTAAGAAGC	ACAAGAGGGA	3420
CAAGCAGAAG	GATCGTAGCG	GCAGCGGTGG	CAGCAAGGAC	AGTTCTCTTC	CCAATGAGCC	3480
TCTGAAGATG	GTTATCAAGA	ATCCCAACGG	CAGCCTGCAG	GCCGGTGCCT	CAGCTCCCAT	3540
TAAACTTAAG	ATCAGCAAAA	ATAAGGTTGA	ACCCAATAAC	TACTCTGCAG	CGGCGGGTCT	3600
GCCTGGCGCA	ATCGGATATG	GCTTGCCCTC	AACTACGGCT	ACCACCACAT	CCGCTTCGAT	3660
CGGAGCAGCT	GCTCCTGTTC	TGCCTCCTTA	TGGTGCCGGC	GGTGGTGGCT	ACAGCTCATC	3720
GGGCGGCAGC	AGTTCCGGTG	GCAGCAGCAA	GAAAAAGCAC	AGCGATCGTG	ACCGCGACAA	3780
GGAGAGCAAA	AAGAATAAGA	GCCAAGACTA	CGCGAAGTAC	AATGGCGCTG	GTGGCGGCAT	3840
CTTTAATCCC	CTTGGCGGTG	CTGGCGCCGC	ACCCAATATG	TCTGGAGGAA	TGGGCGCCCC	3900

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CATGTCTACT GCTGTACCAC CATCCATGCT GTTGGCGCCC ACCGGTGCAG TACCACCCTC 3960
TGCCGCTGGG CTGGCACCGC CTCCCATGCC CGTCTACAAC AAGAAGTAGT GGTAGCGGTC 4020
AGAGGGTTAT TCTTAAGTCG TACGTTTTGA TATATGTATA GAACCTCAGT AAGTCCGATT 4080
GTAGTATAGT TGTTAGGATT GTTAGTGAGA TGCATTATTG ATTTTAGTTA AGCACATAGA 4140
TAAAACTCCA AATTGGAAGT GAAACCGGAT GCGCAGATCG AAGAAGAATG GAAGTAGATG 4200
TCGCGATGGG GCTGGACGTA AAAGCAGTAC TCAAATCGCG AAAACTTTTG TACAGCATTA 4260
ATTAGTTTAT AACTATAATA AATAGCATAC ATATAAGCCC AAAAAAAAAA AAAAAAAAAA 4320
AAAAAAAAA 4328

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1097 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Ser Leu Leu Ala Thr Pro Met Pro Gln Ala Ala Thr Ala Ser Ser
1           5           10           15

Ser Ser Ser Ala Ser Ala Ala Ala Ser Ala Ser Gly Ile Pro Ile Thr
20           25           30

Ala Asn Asn Asn Leu Pro Phe Glu Lys Asp Lys Ile Trp Tyr Phe Ser
35           40           45

Asn Asp Gln Leu Ala Asn Leu Pro Ser Arg Arg Cys Gly Ile Lys Gly
50           55           60

Asp Asp Glu Leu Gln Tyr Arg Gln Met Thr Ala Tyr Leu Ile Gln Glu
65           70           75           80

Met Gly Gln Arg Leu Gln Val Ser Gln Leu Cys Ile Asn Thr Ala Ile
85           90           95

Val Tyr Met His Arg Phe Tyr Ala Phe His Ser Phe Thr His Phe His
100          105          110

Arg Asn Ser Met Ala Ser Ala Ser Leu Phe Leu Ala Ala Lys Val Glu
115          120          125

Glu Gln Pro Arg Lys Leu Glu His Val Ile Arg Ala Ala Asn Lys Cys
130          135          140

Leu Pro Pro Thr Thr Glu Gln Asn Tyr Ala Glu Leu Ala Gln Glu Leu
145          150          155          160

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Val	Phe	Asn	Glu	Asn	Val	Leu	Leu	Gln	Thr	Leu	Gly	Phe	Asp	Val	Ala	
				165					170					175		
Ile	Asp	His	Pro	His	Thr	His	Val	Val	Arg	Thr	Cys	Gln	Leu	Val	Lys	
			180					185					190			
Ala	Cys	Lys	Asp	Leu	Ala	Gln	Thr	Ser	Tyr	Phe	Leu	Ala	Ser	Asn	Ser	
		195					200					205				
Leu	His	Leu	Thr	Ser	Met	Cys	Leu	Gln	Tyr	Arg	Pro	Thr	Val	Val	Ala	
	210					215					220					
Cys	Phe	Cys	Ile	Tyr	Leu	Ala	Cys	Lys	Trp	Ser	Arg	Trp	Glu	Ile	Pro	
225					230					235					240	
Gln	Ser	Thr	Glu	Gly	Lys	His	Trp	Phe	Tyr	Tyr	Val	Asp	Lys	Thr	Val	
				245					250					255		
Ser	Leu	Asp	Leu	Leu	Lys	Gln	Leu	Thr	Asp	Glu	Phe	Ile	Ala	Ile	Tyr	
			260					265					270			
Glu	Lys	Ser	Pro	Ala	Arg	Leu	Lys	Ser	Lys	Leu	Asn	Ser	Ile	Lys	Ala	
		275					280					285				
Ile	Ala	Gln	Gly	Ala	Ser	Asn	Arg	Thr	Ala	Asn	Ser	Lys	Asp	Lys	Pro	
	290					295					300					
Lys	Glu	Asp	Trp	Lys	Ile	Thr	Glu	Met	Met	Lys	Gly	Tyr	His	Ser	Asn	
305					310					315					320	
Ile	Thr	Thr	Pro	Pro	Glu	Leu	Leu	Asn	Gly	Asn	Asp	Ser	Arg	Asp	Arg	
				325					330					335		
Asp	Arg	Asp	Arg	Glu	Arg	Glu	Arg	Glu	Arg	Glu	Arg	Asp	Pro	Ser	Ser	
			340					345					350			
Leu	Leu	Pro	Pro	Pro	Ala	Met	Val	Pro	Gln	Gln	Arg	Arg	Gln	Asp	Gly	
		355					360					365				
Gly	His	Gln	Arg	Ser	Ser	Ser	Val	Ser	Gly	Val	Pro	Gly	Ser	Ser	Ser	
	370					375					380					
Ser	Ser	Ser	Ser	Ser	Ser	His	Lys	Met	Pro	Asn	Tyr	Pro	Gly	Gly	Met	
385					390					395					400	
Pro	Pro	Glu	Ala	His	Pro	Asp	His	Lys	Ser	Lys	Gln	Pro	Gly	Tyr	Asn	
				405					410					415		
Asn	Arg	Met	Pro	Ser	Ser	His	Gln	Arg	Ser	Ser	Ser	Ser	Gly	Leu	Gly	
			420					425					430			
Ser	Ser	Gly	Ser	Gly	Ser	Gln	His	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	
		435					440					445				
Ser	Gln	Gln	Pro	Gly	Arg	Pro	Ser	Met	Pro	Val	Asp	Tyr	His	Lys	Ser	
	450					455					460					

Ser Arg Gly Met Pro Pro Val Gly Val Gly Met Pro Pro His Gly Ser
 465 470 475 480
 His Lys Met Thr Ser Gly Ser Lys Pro Gln Gln Pro Gln Gln Gln Pro
 485 490 495
 Val Pro His Pro Ser Ala Ser Asn Ser Ser Ala Ser Gly Met Ser Ser
 500 505 510
 Lys Asp Lys Ser Gln Ser Asn Lys Met Tyr Pro Asn Ala Pro Pro Pro
 515 520 525
 Tyr Ser Asn Ser Ala Pro Gln Asn Pro Leu Met Ser Arg Gly Gly Tyr
 530 535 540
 Pro Gly Ala Ser Asn Gly Ser Gln Pro Pro Pro Pro Ala Gly Tyr Gly
 545 550 555 560
 Gly His Arg Ser Lys Ser Gly Ser Thr Val His Gly Met Pro His Phe
 565 570 575
 Glu Gln Gln Leu Pro Tyr Ser Gln Ser Gln Ser Tyr Gly His Met Gln
 580 585 590
 Gln Gln Pro Val Pro Gln Ser Gln Gln Gln Gln Met Pro Pro Glu Ala
 595 600 605
 Ser Gln His Ser Leu Gln Ser Lys Asn Ser Leu Phe Ser Pro Glu Trp
 610 615 620
 Pro Asp Ile Lys Lys Glu Pro Met Ser Gln Ser Gln Pro Gln Leu Phe
 625 630 635 640
 Asn Gly Leu Leu Pro Pro Pro Ala Pro Pro Gly His Asp Tyr Lys Leu
 645 650 655
 Asn Ser His Pro Arg Asp Lys Glu Ser Pro Lys Lys Glu Arg Leu Thr
 660 665 670
 Pro Thr Lys Lys Asp Lys His Arg Pro Val Met Pro Pro Met Gly Ser
 675 680 685
 Gly Asn Ser Ser Ser Gly Ser Gly Ser Ser Lys Pro Met Leu Pro Pro
 690 695 700
 His Lys Lys Gln Ile Pro His Gly Gly Asp Leu Leu Thr Asn Pro Gly
 705 710 715 720
 Glu Ser Gly Ser Leu Lys Arg Pro Asn Glu Ile Ser Gly Ser Gln Tyr
 725 730 735
 Gly Leu Asn Lys Leu Asp Glu Ile Asp Asn Ser Asn Met Pro Arg Glu
 740 745 750
 Lys Leu Arg Lys Leu Asp Thr Thr Thr Gly Leu Pro Thr Tyr Pro Asn
 755 760 765

Tyr	Glu	Glu	Lys	His	Thr	Pro	Leu	Asn	Met	Ser	Asn	Gly	Ile	Glu	Thr	770	775	780	
Thr	Pro	Asp	Leu	Val	Arg	Ser	Leu	Leu	Lys	Glu	Ser	Leu	Cys	Pro	Ser	785	790	795	800
Asn	Ala	Ser	Leu	Leu	Lys	Pro	Asp	Ala	Leu	Thr	Met	Pro	Gly	Leu	Lys	805	810	815	
Pro	Pro	Ala	Glu	Leu	Leu	Glu	Pro	Met	Pro	Ala	Pro	Ala	Thr	Ile	Lys	820	825	830	
Lys	Glu	Gln	Gly	Ile	Thr	Pro	Met	Thr	Ser	Leu	Ala	Ser	Gly	Pro	Ala	835	840	845	
Pro	Met	Asp	Leu	Glu	Val	Pro	Thr	Lys	Gln	Ala	Gly	Glu	Ile	Lys	Glu	850	855	860	
Glu	Ser	Ser	Ser	Lys	Ser	Glu	Lys	Lys	Lys	Lys	Lys	Asp	Lys	His	Lys	865	870	875	880
His	Lys	Glu	Lys	Asp	Lys	Ser	Lys	Asp	Lys	Thr	Glu	Lys	Glu	Glu	Arg	885	890	895	
Lys	Lys	His	Lys	Arg	Asp	Lys	Gln	Lys	Asp	Arg	Ser	Gly	Ser	Gly	Gly	900	905	910	
Ser	Lys	Asp	Ser	Ser	Leu	Pro	Asn	Glu	Pro	Leu	Lys	Met	Val	Ile	Lys	915	920	925	
Asn	Pro	Asn	Gly	Ser	Leu	Gln	Ala	Gly	Ala	Ser	Ala	Pro	Ile	Lys	Leu	930	935	940	
Lys	Ile	Ser	Lys	Asn	Lys	Val	Glu	Pro	Asn	Asn	Tyr	Ser	Ala	Ala	Ala	945	950	955	960
Gly	Leu	Pro	Gly	Ala	Ile	Gly	Tyr	Gly	Leu	Pro	Pro	Thr	Thr	Ala	Thr	965	970	975	
Thr	Thr	Ser	Ala	Ser	Ile	Gly	Ala	Ala	Ala	Pro	Val	Leu	Pro	Pro	Tyr	980	985	990	
Gly	Ala	Gly	Gly	Gly	Gly	Tyr	Ser	Ser	Ser	Gly	Gly	Ser	Ser	Ser	Gly	995	1000	1005	
Gly	Ser	Ser	Lys	Lys	Lys	His	Ser	Asp	Arg	Asp	Arg	Asp	Lys	Glu	Ser	1010	1015	1020	
Lys	Lys	Asn	Lys	Ser	Gln	Asp	Tyr	Ala	Lys	Tyr	Asn	Gly	Ala	Gly	Gly	1025	1030	1035	1040
Gly	Ile	Phe	Asn	Pro	Leu	Gly	Gly	Ala	Gly	Ala	Ala	Pro	Asn	Met	Ser	1045	1050	1055	
Gly	Gly	Met	Gly	Ala	Pro	Met	Ser	Thr	Ala	Val	Pro	Pro	Ser	Met	Leu	1060	1065	1070	

Leu Ala Pro Thr Gly Ala Val Pro Pro Ser Ala Ala Gly Leu Ala Pro
1075 1080 1085

Pro Pro Met Pro Val Tyr Asn Lys Lys
1090 1095

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GCA AAG CAG TAC GAC TCG GTG GAG TGC CCT TTT TGT GAT GAA GTT	48
Met Ala Lys Gln Tyr Asp Ser Val Glu Cys Pro Phe Cys Asp Glu Val	
1 5 10 15	
TCC AAA TAC GAG AAG CTC GCC AAG ATC GGC CAA GGC ACC TTC GGG GAG	96
Ser Lys Tyr Glu Lys Leu Ala Lys Ile Gly Gln Gly Thr Phe Gly Glu	
20 25 30	
GTG TTC AAG GCC AGG CAC CGC AAG ACC GGC CAG AAG GTG GCT CTG AAG	144
Val Phe Lys Ala Arg His Arg Lys Thr Gly Gln Lys Val Ala Leu Lys	
35 40 45	
AAG GTG CTG ATG GAA AAC GAG AAG GAG GGG TTC CCC ATT ACA GCC TTG	192
Lys Val Leu Met Glu Asn Glu Lys Glu Gly Phe Pro Ile Thr Ala Leu	
50 55 60	
CGG GAG ATC AAG ATC CTT CAG CTT CTA AAA CAC GAG AAT GTG GTC AAC	240
Arg Glu Ile Lys Ile Leu Gln Leu Leu Lys His Glu Asn Val Val Asn	
65 70 75 80	
TTG ATT GAG ATT TGT CGA ACC AAA GCT TCC CCC TAT AAC CGC TGC AAG	288
Leu Ile Glu Ile Cys Arg Thr Lys Ala Ser Pro Tyr Asn Arg Cys Lys	
85 90 95	
GGT AGT ATA TAC CTG GTG TTC GAC TTC TGC GAG CAT GAC CTT GCT GGG	336
Gly Ser Ile Tyr Leu Val Phe Asp Phe Cys Glu His Asp Leu Ala Gly	
100 105 110	
CTG TTG AGC AAT GTT TTG GTC AAG TTC ACG CTG TCT GAG ATC AAG AGG	384
Leu Leu Ser Asn Val Leu Val Lys Phe Thr Leu Ser Glu Ile Lys Arg	
115 120 125	
GTG ATG CAG ATG CTG CTT AAC GGC CTC TAC TAC ATC CAC AGA AAC AAG	432
Val Met Gln Met Leu Leu Asn Gly Leu Tyr Tyr Ile His Arg Asn Lys	
130 135 140	

ATC CTG CAT AGG GAC ATG AAG GCT GCT AAT GTG CTT ATC ACT CGT GAT	480
Ile Leu His Arg Asp Met Lys Ala Ala Asn Val Leu Ile Thr Arg Asp	
145 150 155 160	
GGG GTC CTG AAG CTG GCA GAC TTT GGG CTG GCC CGG GCC TTC AGC CTG	528
Gly Val Leu Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Ser Leu	
165 170 175	
GCC AAG AAC AGC CAG CCC AAC CGC TAC ACC AAC CGT GTG GTG ACA CTC	576
Ala Lys Asn Ser Gln Pro Asn Arg Tyr Thr Asn Arg Val Val Thr Leu	
180 185 190	
TGG TAC CGG CCC CCG GAG CTG TTG CTC GGG GAG CGG GAC TAC GGC CCC	624
Trp Tyr Arg Pro Pro Glu Leu Leu Leu Gly Glu Arg Asp Tyr Gly Pro	
195 200 205	
CCC ATT GAC CTG TGG GGT GCT GGG TGC ATC ATG GCA GAG ATG TGG ACC	672
Pro Ile Asp Leu Trp Gly Ala Gly Cys Ile Met Ala Glu Met Trp Thr	
210 215 220	
CGC AGC CCC ATC ATG CAG GGC AAC ACG GAG CAG CAC CAA CTC GCC CTC	720
Arg Ser Pro Ile Met Gln Gly Asn Thr Glu Gln His Gln Leu Ala Leu	
225 230 235 240	
ATC AGT CAG CTC TGC GGC TCC ATC ACC CCT GAG GTG TGG CCA AAC GTG	768
Ile Ser Gln Leu Cys Gly Ser Ile Thr Pro Glu Val Trp Pro Asn Val	
245 250 255	
GAC AAC TAT GAG CTG TAC GAA AAG CTG GAG CTG GTC AAG GGC CAG AAG	816
Asp Asn Tyr Glu Leu Tyr Glu Lys Leu Glu Leu Val Lys Gly Gln Lys	
260 265 270	
CGG AAG GTG AAG GAC AGG CTG AAG GCC TAT GTG CGT GAC CCA TAC GCA	864
Arg Lys Val Lys Asp Arg Leu Lys Ala Tyr Val Arg Asp Pro Tyr Ala	
275 280 285	
CTG GAC CTC ATC GAC AAG CTG CTG GTG CTG GAC CCT GCC CAG CGC ATC	912
Leu Asp Leu Ile Asp Lys Leu Leu Val Leu Asp Pro Ala Gln Arg Ile	
290 295 300	
GAC AGC GAT GAC GCC CTC AAC CAC GAC TTC TTC TGG TCC GAC CCC ATG	960
Asp Ser Asp Asp Ala Leu Asn His Asp Phe Phe Trp Ser Asp Pro Met	
305 310 315 320	
CCC TCC GAC CTC AAG GGC ATG CTC TCC ACC CAC CTG ACG TCC ATG TTC	1008
Pro Ser Asp Leu Lys Gly Met Leu Ser Thr His Leu Thr Ser Met Phe	
325 330 335	
GAG TAC TTG GCA CCA CCG CGC CGG AAG GGC AGC CAG ATC ACC CAG CAG	1056
Glu Tyr Leu Ala Pro Pro Arg Arg Lys Gly Ser Gln Ile Thr Gln Gln	
340 345 350	
TCC ACC AAC CAG AGT CGC AAT CCC GCC ACC ACC AAC CAG ACG GAG TTT	1104
Ser Thr Asn Gln Ser Arg Asn Pro Ala Thr Thr Asn Gln Thr Glu Phe	
355 360 365	
GAG CGC GTC TTC TGA	1119

Glu Arg Val Phe

370

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Lys Gln Tyr Asp Ser Val Glu Cys Pro Phe Cys Asp Glu Val
1 5 10 15

Ser Lys Tyr Glu Lys Leu Ala Lys Ile Gly Gln Gly Thr Phe Gly Glu
20 25 30

Val Phe Lys Ala Arg His Arg Lys Thr Gly Gln Lys Val Ala Leu Lys
35 40 45

Lys Val Leu Met Glu Asn Glu Lys Glu Gly Phe Pro Ile Thr Ala Leu
50 55 60

Arg Glu Ile Lys Ile Leu Gln Leu Leu Lys His Glu Asn Val Val Asn
65 70 75 80

Leu Ile Glu Ile Cys Arg Thr Lys Ala Ser Pro Tyr Asn Arg Cys Lys
85 90 95

Gly Ser Ile Tyr Leu Val Phe Asp Phe Cys Glu His Asp Leu Ala Gly
100 105 110

Leu Leu Ser Asn Val Leu Val Lys Phe Thr Leu Ser Glu Ile Lys Arg
115 120 125

Val Met Gln Met Leu Leu Asn Gly Leu Tyr Tyr Ile His Arg Asn Lys
130 135 140

Ile Leu His Arg Asp Met Lys Ala Ala Asn Val Leu Ile Thr Arg Asp
145 150 155 160

Gly Val Leu Lys Leu Ala Asp Phe Gly Leu Ala Arg Ala Phe Ser Leu
165 170 175

Ala Lys Asn Ser Gln Pro Asn Arg Tyr Thr Asn Arg Val Val Thr Leu
180 185 190

Trp Tyr Arg Pro Pro Glu Leu Leu Leu Gly Glu Arg Asp Tyr Gly Pro
195 200 205

Pro Ile Asp Leu Trp Gly Ala Gly Cys Ile Met Ala Glu Met Trp Thr

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: one-of(8, 14)
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "N = A or C or G or T"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "Y = C or T"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: one-of(17, 20)
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "R = A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAATTCNAT GYTNCARCAR CC

22

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: one-of(13, 16, 19, 22, 25)
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "R = A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AACTGCAGTC CARAARAART CRTGRTT

27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGTCAAGGAT CAAACCGGCT GTGAT

25

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAATTCCAA GAAACGCATC GATGC

25

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGACCTGCCA AATCGTGT

18

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AGAAGGTGGA TCTGTAACCA TTCGT

25

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAATTCAGA TCTCGATCAG ATTCA

25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTACTACTCG AGCTACCAAA CCCGGTC

27

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TAAGCAAGCT TCTATGGCGC ACATGTCC

28

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTACTACTCG AGCTACCAAA CCCGGTC

27

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
 - (B) LOCATION: one-of(13, 16, 22)
 - (D) OTHER INFORMATION: /mod_base= OTHER
- /note= "Y = C or T"

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 17
 (D) OTHER INFORMATION: /mod_base= OTHER
/note= "W = A or T"

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 18
 (D) OTHER INFORMATION: /mod_base= OTHER
/note= "S = C or G"

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 19
 (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = A or C or G or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGAATTCTGG TAYTTYWSNA AYGA

24

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /mod_base= OTHER
/note= "Y = C or T"

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: 14
 (D) OTHER INFORMATION: /mod_base= OTHER

/note= "R = A or G"

(ix) FEATURE:
 (A) NAME/KEY: modified_base
 (B) LOCATION: one-of(17, 20)
 (D) OTHER INFORMATION: /mod_base= OTHER
/note= "N = A or C or G or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGGGATCCTG YTCRAANGGN GGCAT

25

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: one-of(11, 14, 20)
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "N = A or C or G or T"

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /mod_base= OTHER

/note= "R = A or G"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGGGATCCAA NGGNGGCATN CCRT

24

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATCACGACAC CACCAGAGCT GTTA

24

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGAATTCAGA TCGTGAACGG GA

22

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGAATTCAGG CGCTAGCAAT G 21

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAAAGGCGTA GAACCGA 17

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCTGACCCAT TTCCTGTATC AGATAG 26

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGAATTCTTC TGCTTGGCGA AT 22

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGGAATTCGA GGTTCCTATAC ATAT 24

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTGTGTGAAT GGAATCTGTG ATGTG

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TATCCCGGGT CATATGAGTC TCCTAGCC

28

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Leu	Gln	Gln	Pro	Ser	Gly	Ser	Thr	Pro	Ser	Asn	Val
1				5					10			

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ala	Asp	Thr	Ala	Leu	Asn	His	Asp	Phe	Phe	Trp	Thr	Asp	Pro	Met	Pro
1				5					10					15	

Ser

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Leu Gln Gln Pro
1 5

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asn His Asp Phe Phe Trp Thr
1 5

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ser Pro Glu Trp Pro Asp Ile
1 5

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Trp Tyr Phe Ser Asn Asp Gln Leu Ala Asn Ser Pro Ser Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Thr Val His Gly Met Pro Pro Phe Glu Gln Gln Leu Pro Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Trp Tyr Phe Ser Asn Asp
1 5

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Pro Pro Phe Glu Gln
1 5

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

His Gly Met Pro Pro Phe
1 5

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 41 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCAGGATCCA GAATTCCATA TGGCAAAGCA GTACGACTCG G 41

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CAGTACTCGA GTTATCAGAA GACGCGCTCA AAC 33

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4528 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGGGGGGGGG GGGTGAATGA AGGAGCGGGC GGAGGAGGAA TTGTCATGGC GTCGGGCCGT 60
GGAGCTTCTT CTCGCTGGTT CTTTACTCGG GAACAGCTGG AGAACACGCC GAGCCGCCGC 120
TGCGGAGTGG AGGCGGATAA AGAGCTCTCG TGCCGCCAGC AGGCGGCCAA CCTCATCCAG 180
GAGATGGGAC AGCGTCTCAA TGTCTCTCAG CTTACAATAA AACTGCGAT TGTTTATATG 240
CACAGGTTTT ATATGCACCA TTCTTTCACC AAATTCAACA AAAATATAAT ATCGTCTACT 300
GCATTATTTT TGGCTGCAAA AGTGAAGAA CAGGCTCGAA AACTTGAACA TGTTATCAAA 360
GTAGCACATG CTTGTCTTCA TCCTCTAGAG CCACTGCTGG ATACTAAATG TGATGCTTAC 420
CTTCAACAGA CTCAAGAACT GGTTATACTT GAAACCATAA TGCTACAAAC TCTAGGTTTT 480
GAGATCACCA TTGAACACCC ACACACAGAT GTGGTGAAAT GTACCCAGTT AGTAAGAGCA 540
AGCAAGGATT TGGCACAGAC ATCCTATTTT ATGGCTACCA ACAGTCTGCA TCTTACAACC 600
TTCTGTCTTC AGTACAAACC AACAGTGATA GCATGTGTAT GCATTCATTT GGCTTGCAAA 660
TGGTCCAATT GGGAGATCCC TGTATCAACT GATGGAAAGC ATTGGTGGGA ATATGTGGAT 720

CCTACAGTTA CTCTAGAATT ATTAGATGAG CTAACACATG AGTTTCTACA AATATTGGAG	780
AAAACGCCTA ATAGGTTGAA GAAGATTCGA AACTGGAGGG CTAATCAGGC AGCTAGGAAA	840
CCAAAAGTAG ATGGACAGGT ATCAGAGACA CCACTTCTTG GTTCATCTTT GGTCCAGAAT	900
TCCATTTTAG TAGATAGTGT CACTGGTGTG CCTACAAACC CAAGTTTTC AAGAACCATCT	960
ACATCAGCAT TCCCTGCGCC AGTACCTCTA AATTCAGGAA ATATTTCTGT TCAAGACAGC	1020
CATACATCTG ATAATTTGTC AATGCTAGCA ACAGGAATGC CAAGTACTTC ATACGGTTTA	1080
TCATCACACC AGGAATGGCC TCAACATCAA GACTCAGCAA GGACAGAACA GCTATATTCA	1140
CAGAAACAGG AGACATCTTT GTCTGGTAGC CAGTACAACA TCAACTTCCA GCAGGGACCT	1200
TCTATATCAC TGCATTCAGG ATTACATCAC AGACCTGACA AAATTTTCAGA TCATTCTTCT	1260
GTTAAGCAAG AATATACTCA TAAAGCAGGG AGCAGTAAAC ACCATGGGCC AATTTCCACT	1320
ACTCCAGGAA TAATTCCTCA GAAAATGTCT TTAGATAAAT ATAGAGAAAA GCGTAAACTA	1380
GAAACTCTTG ATCTCGATGT AAGGGATCAT TATATAGCTG CCCAGGTAGA ACAGCAGCAC	1440
AAACAAGGGC AGTCACAGGC AGCCAGCAGC AGTTCTGTTA CTTCTCCCAT TAAAATGAAA	1500
ATACCTATCG CAAATACTGA AAAATACATG GCAGATAAAA AGGAAAAGAG TGGGTCACTG	1560
AAATTACGGA TTCCAATACC ACCCACTGAT AAAAGCGCCA GTAAAGAAGA ACTGAAAATG	1620
AAAATAAAAG TTTCTTCTTC AGAAAGACAC AGCTCTTCTG ATGAAGGCAG TGGGAAAAGC	1680
AAACATTCAA GCCCACATAT TAGCAGAGAC CATAAGGAGA AGCACAAGGA GCATCCTTCA	1740
AGCCGCCACC ACACCAGCAG CCACAAGCAT TCCCCTCGC ATAGTGGCAG CAGCAGCGGT	1800
GGCAGTAAAC ACAGTGCCGA CGGAATACCA CCCACTGTTC TGAGGAGTCC TGTGCGCTG	1860
AGCAGTGATG GCATTTCTCT TAGCTCCAGC TCTTCAAGGA AGAGGCTGCA TGTCATGAT	1920
GCATCTCACA ACCACCACTC CAAAATGAGC AAAAGTTCCA AAAGTTCAGG TGGGCTACGG	1980
ACATCTCAGC ACCTCGTGAA ACTGGACAAG AAGCCAGTGG AGACCAACGG TCCTGATGCC	2040
AATCACGAGT ACAGTACAAG CAGCCAGCAT ATGGACTACA AAGACACATT CGACATGCTG	2100
GACTCACTGT TAAGTGCCCA AGGAATGAAC ATGTAATAAT TTGTTTAGGT CAATTTTCTC	2160
TTTACTTTTT TAATTTAAAA ATTGTTAGAA TGGAAAAATT CCTTCTGATC TAGCAGTGGT	2220
AACCCCTGCT GTTGCTGCCA CTGCTTCAAT ATTTGTAAGT GCTACTTTAT TCTTCATTCT	2280
GAAAAGAAGA GATTATAGTA AACAAGTCTT TATCTCCACA TATGATAGTG TTATAAATAC	2340
TGTAAAGGCA TGGAAGGTGC AAAACTCAGT ATTTCTACAA TTGCAGCTAA GAACATTAGG	2400

ATGAATGGCT	GGCTGCTTCT	AGGAATATAA	GATGCCTCAA	GCATTCATTA	TTTATGATTT	2460
GAATACTGTA	GCTATTTTTT	GTTGCTTGGC	TTTTGAATGA	GTGTAAATTG	TTTTCTTTTG	2520
TGTATTTATA	CTTGTATGTA	TGATTTGCAT	GTTTCAATGA	TAAAGGGATA	AAACAGTATA	2580
CTGACAACTG	TTTACAAGAA	AGTGGAGAAA	ATGTACTACA	TTTTGTATGT	TTAGATATTA	2640
CCGTAAATAC	TCAGGATTGG	AGCTGCTTGT	AAGTATAACA	ATATACAGAA	TACTTTATTT	2700
TATCTTGTC	GAGTTCCATC	ACTATCTAAA	ACAAAGGTGC	AATTTTTTAT	GTTAACCTTA	2760
AATCTAGCCC	TTACTGGAAG	CCACTGATAG	GGACATTCAC	TACCAGATGT	GTGCAGTGCA	2820
GCAGATGGTC	ATATAACACT	GTGAGGCACT	GAATTTTGCC	TTCAGAGGTT	CTGACCAGAT	2880
TGGCTGCTGA	AATAGCCCCT	AACTTTCTGA	AGGCTTGAAG	AGGAAAAAAT	AAAGTTTACA	2940
TACTCTTGAT	GGAAGTGCAT	TTAAATGTTT	GTTGGCTTGT	TGCAGTTCTA	TGAAACAGAG	3000
CTGTTAATAA	TGGTTATGTG	GATTACTGTG	ATTTGAAAAC	TAAATTCACA	ATAACTTACC	3060
TAGTAGAGAT	TTAGTGAGTT	GTTTCCTTTA	AAGAATTTTA	CACTACATAT	TTTAATAGTA	3120
AACAGGGTCA	CTTTCCTTTA	GCATTCAGAA	TGACACCATA	TTCTTAAATA	TACTCCTTCC	3180
CTGAAGCGTG	TTTGTGTGTG	ATGCCATATT	TCTTTTTTCT	GTAAATGTAG	TCTTCCTTAT	3240
AAAAATGAAA	TTAAACCTAT	GCTCTCAATT	CTTTTATATT	CTAACAATAA	ATAAAAAAGA	3300
AAAGATTACT	GACTGTGCAT	TGTACCTGTA	TTTATAGTTT	ATGGTTATCA	GAAGCTCTGT	3360
AAGAAAGAAA	AGGTCAGCTC	CCAGGCAAAC	CAGTAGTGGA	GGTTTTACAT	TTGTTTGCAC	3420
ATCTCAGTAT	ATTTCTGTTG	AGGTAAAGTT	TGCACAGTCA	TCTGACTTCT	GATCAAGCAT	3480
TAGATTTTAA	CTTGTTTAGA	TTTTGTCTTA	AACACCAGTA	ATATGGCTCT	TGTTTATCAG	3540
CTAATCTTGA	ATTTATTCTG	TGGTAAATCT	TTTGAGTTGC	TGAGTATATT	TGAGATTGAT	3600
TGGATTCAAC	CTCTTGTTGA	ACTGAAAAC	TAATTTTTTC	TCTGTATTTT	TGTTACAAAG	3660
CCACTGATAC	GTGCACAATT	GTAATTAAGT	ATGTTGCAGT	TGTAAATATT	AGAGTTTAAT	3720
CTCATGCTCT	ACCTTTATTT	AGCAATTACC	TAATTTGCCA	GTAGCTTTAT	AATTTTTTAA	3780
GATAATTGTT	CATTATTTTG	TCAATGTTAT	TTGAACTTGG	GGTACTTAGG	AGCCTCTTTG	3840
TAGGGACTGT	GCCTAGGTAG	CATGTCCTAA	CATTTGTTCT	GGTCTTGCAT	AACTTCAGTA	3900
TCTTTGTCAT	TATATGTAAC	TTTGTTGCTC	TGTATGGCAT	AATATTGTAT	CCATAAACAT	3960
GGTAATTTTG	ATACAGTTAT	ACTTTTACAG	TGGTACATAA	TCCAAGGACT	AGTATAGAAT	4020
TAAGCTGAGT	GCAAGATGAG	GGAGGGAAGG	GCTTTCTTGG	TAATTTAGAT	GTGAAACCTC	4080
TACAGAGCTA	TCATGTAAAA	ACTACATGAG	GTGGTTGTGC	TACTGTATAA	TTGGGGGTGA	4140

TAATACCAGG AATTTTAATA AGATTTTGTA AAGAATATCC AGAAAAGTAG TGAACCTTATT	4200
TTCAGTAGGC ATAGAAAACA ATGTGAATAT TTAAGGTCTG TGAATATAGT TAAACTTCAC	4260
TAAGAATTTG CAGAATTGTT TTGAGATGTG TGAATAAAGG TAATTTTATT GAATCTTCAT	4320
TGGTGCTAAT GTTGACAGT TAAAAAGATA GCTAGTGAT ATTGTTATGG GTCAGTACTT	4380
ATTAGTACTT CCAAATTGA ATTTGAAATG CTATGTATTC ACTTTTCACT CTGTAAATGT	4440
AATTCTTTAC AATGACTTTA TTTATTAAAG GGCAGCCAGT TGTCATTTGT AAAAAAAAAA	4500
AAAAAAAAAA AAAGCGGCCG CTGAATTC	4528

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2091 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATGGCGTCGG GCCGTGGAGC TTCTTCTCGC TGGTTCTTTA CTCGGGAACA GCTGGAGAAC	60
ACGCCGAGCC GCCGCTGCGG AGTGGAGGCG GATAAAGAGC TCTCGTGCCG CCAGCAGGCG	120
GCCAACCTCA TCCAGGAGAT GGGACAGCGT CTCAATGTCT CTCAGCTTAC AATAAACACT	180
GCGATTGTTT ATATGCACAG GTTTTATATG CACCATTCTT TCACCAAATT CAACAAAAT	240
ATAATATCGT CTAATGCATT ATTTTGGCT GCAAAAGTGG AAGAACAGGC TCGAAACTT	300
GAACATGTTA TCAAAGTAGC ACATGCTTGT CTTTCATCTC TAGAGCCACT GCTGGATACT	360
AAATGTGATG CTTACCTTCA ACAGACTCAA GAACTGGTTA TACTTGAAAC CATAATGCTA	420
CAAACTCTAG GTTTTGAGAT CACCATTGAA CACCCACACA CAGATGTGGT GAAATGTACC	480
CAGTTAGTAA GAGCAAGCAA GGATTTGGCA CAGACATCCT ATTTTCATGGC TACCAACAGT	540
CTGCATCTTA CAACCTTCTG TCTTCAGTAC AAACCAACAG TGATAGCATG TGTATGCATT	600
CATTTGGCTT GCAAATGGTC CAATTGGGAG ATCCCTGTAT CAACTGATGG AAAGCATTGG	660
TGGGAATATG TGGATCCTAC AGTTACTCTA GAATTATTAG ATGAGCTAAC ACATGAGTTT	720
CTACAAATAT TGGAGAAAAC GCCTAATAGG TTGAAGAAGA TTCGAACTG GAGGGCTAAT	780
CAGGCAGCTA GGAAACCAAA AGTAGATGGA CAGGTATCAG AGACACCACT TCTTGGTTCA	840
TCTTTGGTCC AGAATTCCAT TTTAGTAGAT AGTGTCCTG GTGTGCCTAC AAACCAAGT	900
TTTCAGAAAC CATCTACATC AGCATTCCCT GCGCCAGTAC CTCTAAATTC AGGAAATATT	960

TCTGTTCAAG ACAGCCATAC ATCTGATAAT TTGTCAATGC TAGCAACAGG AATGCCAAGT 1020
 ACTTCATACG GTTTATCATC ACACCAGGAA TGGCCTCAAC ATCAAGACTC AGCAAGGACA 1080
 GAACAGCTAT ATTACAGAA ACAGGAGACA TCTTTGTCTG GTAGCCAGTA CAACATCAAC 1140
 TTCCAGCAGG GACCTTCTAT ATCACTGCAT TCAGGATTAC ATCACAGACC TGACAAAATT 1200
 TCAGATCATT CTTCTGTTAA GCAAGAATAT ACTCATAAAG CAGGGAGCAG TAAACACCAT 1260
 GGGCCAATTT CCACTACTCC AGGAATAATT CCTCAGAAAA TGTCTTTAGA TAAATATAGA 1320
 GAAAAGCGTA AACTAGAAAC TCTTGATCTC GATGTAAGGG ATCATTATAT AGCTGCCCAG 1380
 GTAGAACAGC AGCACAAACA AGGGCAGTCA CAGGCAGCCA GCAGCAGTTC TGTTACTTCT 1440
 CCCATTAAAA TGAAAATACC TATCGCAAAT ACTGAAAAAT ACATGGCAGA TAAAAAGGAA 1500
 AAGAGTGGGT CACTGAAATT ACGGATTCCA ATACCACCCA CTGATAAAAG CGCCAGTAAA 1560
 GAAGAACTGA AAATGAAAAT AAAAGTTTCT TCTTCAGAAA GACACAGCTC TTCTGATGAA 1620
 GGCAGTGGGA AAAGCAAACA TTCAAGCCCA CATATTAGCA GAGACCATAA GGAGAAGCAC 1680
 AAGGAGCATC CTTCAAGCCG CCACCACACC AGCAGCCACA AGCATTCCCA CTCGCATAGT 1740
 GGCAGCAGCA GCGGTGGCAG TAAACACAGT GCCGACGGAA TACCACCCAC TGTTCTGAGG 1800
 AGTCCTGTTG GCCTGAGCAG TGATGGCATT TCCTCTAGCT CCAGCTCTTC AAGGAAGAGG 1860
 CTGCATGTCA ATGATGCATC TCACAACCAC CACTCCAAAA TGAGCAAAG TTCCAAAAGT 1920
 TCAGGTGGGC TACGGACATC TCAGCACCTC GTGAAACTGG ACAAGAAGCC AGTGGAGACC 1980
 AACGGTCCTG ATGCCAATCA CGAGTACAGT ACAAGCAGCC AGCATATGGA CTACAAAGAC 2040
 ACATTCGACA TGCTGGACTC ACTGTTAAGT GCCCAAGGAA TGAACATGTA A 2091

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Ala Ser Gly Arg Gly Ala Ser Ser Arg Trp Phe Phe Thr Arg Glu
 1 5 10 15

Gln Leu Glu Asn Thr Pro Ser Arg Arg Cys Gly Val Glu Ala Asp Lys
 20 25 30

Glu Leu Ser Cys Arg Gln Gln Ala Ala Asn Leu Ile Gln Glu Met Gly

35						40					45					
Gln	Arg	Leu	Asn	Val	Ser	Gln	Leu	Thr	Ile	Asn	Thr	Ala	Ile	Val	Tyr	
50						55				60						
Met	His	Arg	Phe	Tyr	Met	His	His	Ser	Phe	Thr	Lys	Phe	Asn	Lys	Asn	
65					70					75					80	
Ile	Ile	Ser	Ser	Thr	Ala	Leu	Phe	Leu	Ala	Ala	Lys	Val	Glu	Glu	Gln	
				85						90						
Ala	Arg	Lys	Leu	Glu	His	Val	Ile	Lys	Val	Ala	His	Ala	Cys	Leu	His	
			100						105				110			
Pro	Leu	Glu	Pro	Leu	Leu	Asp	Thr	Lys	Cys	Asp	Ala	Tyr	Leu	Gln	Gln	
		115						120				125				
Thr	Gln	Glu	Leu	Val	Ile	Leu	Glu	Thr	Ile	Met	Leu	Gln	Thr	Leu	Gly	
		130						135				140				
Phe	Glu	Ile	Thr	Ile	Glu	His	Pro	His	Thr	Asp	Val	Val	Lys	Cys	Thr	
145						150						155		160		
Gln	Leu	Val	Arg	Ala	Ser	Lys	Asp	Leu	Ala	Gln	Thr	Ser	Tyr	Phe	Met	
				165						170						
Ala	Thr	Asn	Ser	Leu	His	Leu	Thr	Thr	Phe	Cys	Leu	Gln	Tyr	Lys	Pro	
			180						185				190			
Thr	Val	Ile	Ala	Cys	Val	Cys	Ile	His	Leu	Ala	Cys	Lys	Trp	Ser	Asn	
		195						200				205				
Trp	Glu	Ile	Pro	Val	Ser	Thr	Asp	Gly	Lys	His	Trp	Trp	Glu	Tyr	Val	
		210						215				220				
Asp	Pro	Thr	Val	Thr	Leu	Glu	Leu	Leu	Asp	Glu	Leu	Thr	His	Glu	Phe	
225						230						235		240		
Leu	Gln	Ile	Leu	Glu	Lys	Thr	Pro	Asn	Arg	Leu	Lys	Lys	Ile	Arg	Asn	
				245						250						
Trp	Arg	Ala	Asn	Gln	Ala	Ala	Arg	Lys	Pro	Lys	Val	Asp	Gly	Gln	Val	
			260						265				270			
Ser	Glu	Thr	Pro	Leu	Leu	Gly	Ser	Ser	Leu	Val	Gln	Asn	Ser	Ile	Leu	
		275						280				285				
Val	Asp	Ser	Val	Thr	Gly	Val	Pro	Thr	Asn	Pro	Ser	Phe	Gln	Lys	Pro	
		290						295				300				
Ser	Thr	Ser	Ala	Phe	Pro	Ala	Pro	Val	Pro	Leu	Asn	Ser	Gly	Asn	Ile	
305						310						315		320		
Ser	Val	Gln	Asp	Ser	His	Thr	Ser	Asp	Asn	Leu	Ser	Met	Leu	Ala	Thr	
				325						330						
Gly	Met	Pro	Ser	Thr	Ser	Tyr	Gly	Leu	Ser	Ser	His	Gln	Glu	Trp	Pro	

340	345	350
Gln His Gln Asp Ser Ala Arg Thr Glu Gln Leu Tyr Ser Gln Lys Gln		
355	360	365
Glu Thr Ser Leu Ser Gly Ser Gln Tyr Asn Ile Asn Phe Gln Gln Gly		
370	375	380
Pro Ser Ile Ser Leu His Ser Gly Leu His His Arg Pro Asp Lys Ile		
385	390	395
Ser Asp His Ser Ser Val Lys Gln Glu Tyr Thr His Lys Ala Gly Ser		
405	410	415
Ser Lys His His Gly Pro Ile Ser Thr Thr Pro Gly Ile Ile Pro Gln		
420	425	430
Lys Met Ser Leu Asp Lys Tyr Arg Glu Lys Arg Lys Leu Glu Thr Leu		
435	440	445
Asp Leu Asp Val Arg Asp His Tyr Ile Ala Ala Gln Val Glu Gln Gln		
450	455	460
His Lys Gln Gly Gln Ser Gln Ala Ala Ser Ser Ser Ser Val Thr Ser		
465	470	475
Pro Ile Lys Met Lys Ile Pro Ile Ala Asn Thr Glu Lys Tyr Met Ala		
485	490	495
Asp Lys Lys Glu Lys Ser Gly Ser Leu Lys Leu Arg Ile Pro Ile Pro		
500	505	510
Pro Thr Asp Lys Ser Ala Ser Lys Glu Glu Leu Lys Met Lys Ile Lys		
515	520	525
Val Ser Ser Ser Glu Arg His Ser Ser Ser Asp Glu Gly Ser Gly Lys		
530	535	540
Ser Lys His Ser Ser Pro His Ile Ser Arg Asp His Lys Glu Lys His		
545	550	555
Lys Glu His Pro Ser Ser Arg His His Thr Ser Ser His Lys His Ser		
565	570	575
His Ser His Ser Gly Ser Ser Ser Gly Gly Ser Lys His Ser Ala Asp		
580	585	590
Gly Ile Pro Pro Thr Val Leu Arg Ser Pro Val Gly Leu Ser Ser Asp		
595	600	605
Gly Ile Ser Ser Ser Ser Ser Ser Ser Arg Lys Arg Leu His Val Asn		
610	615	620
Asp Ala Ser His Asn His His Ser Lys Met Ser Lys Ser Ser Lys Ser		
625	630	635
Ser Gly Gly Leu Arg Thr Ser Gln His Leu Val Lys Leu Asp Lys Lys		

	645		650		655
Pro Val Glu Thr Asn Gly Pro Asp Ala Asn His Glu Tyr Ser Thr Ser					
	660		665		670
Ser Gln His Met Asp Tyr Lys Asp Thr Phe Asp Met Leu Asp Ser Leu					
	675		680		685
Leu Ser Ala Gln Gly Met Asn Met					
	690		695		

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATGGCGTCGG GCCGTGGAGC TTCTTCTCGC TGGTTCTTTA CTCGGGAACA GCTGGAGAAC	60
ACGCCGAGCC GCCGCTGCGG AGTGGAGGCG GATAAAGAGC TCTCGTGCCG CCAGCAGGCG	120
GCCAACTCA TCCAGGAGAT GGGACAGCGT CTCAATGTCT CTCAGCTTAC AATAAACACT	180
GCGATTGTTT ATATGCACAG GTTTTATATG CACCATTCTT TCACCAAATT CAACAAAAT	240
ATAATATCGT CTACTGCATT ATTTTGGCT GCAAAGTGG AAGAACAGGC TCGAAAATT	300
GAACATGTTA TCAAAGTAGC ACATGCTTGT CTTTCATCTC TAGAGCCACT GCTGGATACT	360
AAATGTGATG CTTACCTTCA ACAGACTCAA GAACTGGTTA TACTTGAAAC CATAATGCTA	420
CAAACCTTAG GTTTTGAGAT CACCATTGAA CACCCACACA CAGATGTGGT GAAATGTACC	480
CAGTTAGTAA GAGCAAGCAA GGATTTGGCA CAGACATCCT ATTTTCATGGC TACCAACAGT	540
CTGCATCTTA CAACCTTCTG TCTTCAGTAC AAACCAACAG TGATAGCATG TGTATGCATT	600
CATTTGGCTT GCAAATGGTC CAATTGGGAG ATCCCTGTAT CAACTGATGG AAAGCATTGG	660
TGGGAATATG TGGATCCTAC AGTTACTCTA GAATTATTAG ATGAGCTAAC ACATGAGTTT	720
CTACAAATAT TGGAGAAAAC GCCTAATAGG TTGAAGAAGA TTCGAACTG GAGGGCTAAT	780
CAGGCAGCTA GGAAACCAA AGTAGATGGA CAGGTATCAG AGACACCACT TCTTGGTTCA	840
TCTTTGGTCC AGAATTCCAT TTTAGTAGAT AGTGTCCTG GTGTGCCTAC AAACCCAAGT	900
TTTCAGAAAC CATCTACATC AGCATTCCCT GCGCCAGTAC CTCTAAATTC AGGAAATATT	960
TCTGTTCAAG ACAGCCATAC ATCTGATAAT TTGTCAATGC TAGCAACAGG AATGCCAAGT	1020
ACTTCATACG GTTTATCATC ACACCAGGAA TGGCCTCAAC ATCAAGACTC AGCAAGGACA	1080

GAACAGCTAT ATTACAGAA ACAGGAGACA TCTTTGTCTG GTAGCCAGTA CAACATCAAC 1140
 TTCCAGCAGG GACCTTCTAT ATCACTGCAT TCAGGATTAC ATCACAGACC TGACAAAATT 1200
 TCAGATCATT CTTCTGTAA GCAGGAATAT ACTCATAAAG CAGGGAGCAG TAAACACCAT 1260
 GGGCCAATTT CCACTACTCC AGGAATAATT CCTCAGAAAA TGTCTTTAGA TAAATATAGA 1320
 GAAAAGCGTA AACTAGAAAC TCTTGATCTC GATGTAAGGG ATCATTATAT AGCTGCCCAG 1380
 GTAGAACAGC AGCACAAACA AGGGCAGTCA CAGGCAGCCA GCAGCAGTTC TGTTACTTCT 1440
 CCCATTAAAA TGAAAATACC TATCGCAAAT ACTGAAAAAT ACATGGCAGA TAAAAAGGAA 1500
 AAGAGTGGGT CACTGAAATT ACGGATTCCA ATACCACCCA CTGATAAAAG CGCCAGTAAA 1560
 GAAGAACTGA AAATGAAAAT AAAAGTTTCT TCTTCAGAAA GACACAGCTC TTCTGATGAA 1620
 GGCAGTGGGA AAAGCAAACA TTCAAGCCCA CATATTAGCA GAGACCATAA GGAGAAGCAC 1680
 AAGGAGCATC CTTCAAGCCG CCACCACACC AGCAGCCACA AGCATTCCCA CTCGCATAGT 1740
 GGCAGCAGCA GCGGTGGCAG TAAACACAGT GCCGACGGAA TACCACCCAC TGTTCTGAGG 1800
 AGTCCTGTTG GCCTGAGCAG TGATGGCATT TCCTCTAGCT CCAGCTCTTC AAGGAAGAGG 1860
 CTGCATGTCA ATGATGCATC TCACAACCAC CACTCCAAAA TGAGCAAAAG TTCCAAAAGT 1920
 TCAGGTAGTT CATCTAGTTC TTCCTCCTCT GTTAAGCAGT ATATATCCTC TCACAACTCT 1980
 GTTTTTAACC ATCCCTTACC CCTCCTCCCC TGTCACATAC CAGGTGGGCT ACGGACATCT 2040
 CTGCACCTCG TGAAACTGGA CAAGAAGCCA GTGGAGACCA ACGGTCCTGA TGCCAATCAC 2100
 GAGTACAGTA CAAGCAGCCA GCATATGGAC TACAAAGACA CATTGACAT GCTGGACTCA 2160
 CTGTTAAGTG CCAAGGAAT GAACATGTAA 2190

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Ala Ser Gly Arg Gly Ala Ser Ser Arg Trp Phe Phe Thr Arg Glu
 1 5 10 15
 Gln Leu Glu Asn Thr Pro Ser Arg Arg Cys Gly Val Glu Ala Asp Lys
 20 25 30
 Glu Leu Ser Cys Arg Gln Gln Ala Ala Asn Leu Ile Gln Glu Met Gly

35					40					45					
Gln	Arg	Leu	Asn	Val	Ser	Gln	Leu	Thr	Ile	Asn	Thr	Ala	Ile	Val	Tyr
50					55					60					
Met	His	Arg	Phe	Tyr	Met	His	His	Ser	Phe	Thr	Lys	Phe	Asn	Lys	Asn
65					70					75					80
Ile	Ile	Ser	Ser	Thr	Ala	Leu	Phe	Leu	Ala	Ala	Lys	Val	Glu	Glu	Gln
				85					90					95	
Ala	Arg	Lys	Leu	Glu	His	Val	Ile	Lys	Val	Ala	His	Ala	Cys	Leu	His
			100					105					110		
Pro	Leu	Glu	Pro	Leu	Leu	Asp	Thr	Lys	Cys	Asp	Ala	Tyr	Leu	Gln	Gln
		115					120					125			
Thr	Gln	Glu	Leu	Val	Ile	Leu	Glu	Thr	Ile	Met	Leu	Gln	Thr	Leu	Gly
	130					135					140				
Phe	Glu	Ile	Thr	Ile	Glu	His	Pro	His	Thr	Asp	Val	Val	Lys	Cys	Thr
145					150					155					160
Gln	Leu	Val	Arg	Ala	Ser	Lys	Asp	Leu	Ala	Gln	Thr	Ser	Tyr	Phe	Met
				165					170					175	
Ala	Thr	Asn	Ser	Leu	His	Leu	Thr	Thr	Phe	Cys	Leu	Gln	Tyr	Lys	Pro
			180					185					190		
Thr	Val	Ile	Ala	Cys	Val	Cys	Ile	His	Leu	Ala	Cys	Lys	Trp	Ser	Asn
		195					200					205			
Trp	Glu	Ile	Pro	Val	Ser	Thr	Asp	Gly	Lys	His	Trp	Trp	Glu	Tyr	Val
	210					215					220				
Asp	Pro	Thr	Val	Thr	Leu	Glu	Leu	Leu	Asp	Glu	Leu	Thr	His	Glu	Phe
225					230					235					240
Leu	Gln	Ile	Leu	Glu	Lys	Thr	Pro	Asn	Arg	Leu	Lys	Lys	Ile	Arg	Asn
				245					250					255	
Trp	Arg	Ala	Asn	Gln	Ala	Ala	Arg	Lys	Pro	Lys	Val	Asp	Gly	Gln	Val
			260					265					270		
Ser	Glu	Thr	Pro	Leu	Leu	Gly	Ser	Ser	Leu	Val	Gln	Asn	Ser	Ile	Leu
		275					280					285			
Val	Asp	Ser	Val	Thr	Gly	Val	Pro	Thr	Asn	Pro	Ser	Phe	Gln	Lys	Pro
	290					295					300				
Ser	Thr	Ser	Ala	Phe	Pro	Ala	Pro	Val	Pro	Leu	Asn	Ser	Gly	Asn	Ile
305					310					315					320
Ser	Val	Gln	Asp	Ser	His	Thr	Ser	Asp	Asn	Leu	Ser	Met	Leu	Ala	Thr
				325					330					335	

Gly	Met	Pro	Ser	Thr	Ser	Tyr	Gly	Leu	Ser	Ser	His	Gln	Glu	Trp	Pro	340	345	350	
Gln	His	Gln	Asp	Ser	Ala	Arg	Thr	Glu	Gln	Leu	Tyr	Ser	Gln	Lys	Gln	355	360	365	
Glu	Thr	Ser	Leu	Ser	Gly	Ser	Gln	Tyr	Asn	Ile	Asn	Phe	Gln	Gln	Gly	370	375	380	
Pro	Ser	Ile	Ser	Leu	His	Ser	Gly	Leu	His	His	Arg	Pro	Asp	Lys	Ile	385	390	395	400
Ser	Asp	His	Ser	Ser	Val	Lys	Gln	Glu	Tyr	Thr	His	Lys	Ala	Gly	Ser	405	410	415	
Ser	Lys	His	His	Gly	Pro	Ile	Ser	Thr	Thr	Pro	Gly	Ile	Ile	Pro	Gln	420	425	430	
Lys	Met	Ser	Leu	Asp	Lys	Tyr	Arg	Glu	Lys	Arg	Lys	Leu	Glu	Thr	Leu	435	440	445	
Asp	Leu	Asp	Val	Arg	Asp	His	Tyr	Ile	Ala	Ala	Gln	Val	Glu	Gln	Gln	450	455	460	
His	Lys	Gln	Gly	Gln	Ser	Gln	Ala	Ala	Ser	Ser	Ser	Ser	Val	Thr	Ser	465	470	475	480
Pro	Ile	Lys	Met	Lys	Ile	Pro	Ile	Ala	Asn	Thr	Glu	Lys	Tyr	Met	Ala	485	490	495	
Asp	Lys	Lys	Glu	Lys	Ser	Gly	Ser	Leu	Lys	Leu	Arg	Ile	Pro	Ile	Pro	500	505	510	
Pro	Thr	Asp	Lys	Ser	Ala	Ser	Lys	Glu	Glu	Leu	Lys	Met	Lys	Ile	Lys	515	520	525	
Val	Ser	Ser	Ser	Glu	Arg	His	Ser	Ser	Ser	Asp	Glu	Gly	Ser	Gly	Lys	530	535	540	
Ser	Lys	His	Ser	Ser	Pro	His	Ile	Ser	Arg	Asp	His	Lys	Glu	Lys	His	545	550	555	560
Lys	Glu	His	Pro	Ser	Ser	Arg	His	His	Thr	Ser	Ser	His	Lys	His	Ser	565	570	575	
His	Ser	His	Ser	Gly	Ser	Ser	Ser	Gly	Gly	Ser	Lys	His	Ser	Ala	Asp	580	585	590	
Gly	Ile	Pro	Pro	Thr	Val	Leu	Arg	Ser	Pro	Val	Gly	Leu	Ser	Ser	Asp	595	600	605	
Gly	Ile	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Arg	Lys	Arg	Leu	His	Val	Asn	610	615	620	
Asp	Ala	Ser	His	Asn	His	His	Ser	Lys	Met	Ser	Lys	Ser	Ser	Lys	Ser	625	630	635	640

Ser Gly Ser Ser Ser Ser Ser Ser Ser Ser Val Lys Gln Tyr Ile Ser
 645 650 655
 Ser His Asn Ser Val Phe Asn His Pro Leu Pro Leu Leu Pro Cys His
 660 665 670
 Ile Pro Gly Gly Leu Arg Thr Ser Gln His Leu Val Lys Leu Asp Lys
 675 680 685
 Lys Pro Val Glu Thr Asn Gly Pro Asp Ala Asn His Glu Tyr Ser Thr
 690 695 700
 Ser Ser Gln His Met Asp Tyr Lys Asp Thr Phe Asp Met Leu Asp Ser
 705 710 715 720
 Leu Leu Ser Ala Gln Gly Met Asn Met
 725

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GGAAGTGCCT GCAACCTTCG CCGCTGCCTT CTGGTTGAAG CACTATGGAG GGAGAGAGGA	60
AGAACAACAA CAAACGGTGG TATTTCACTC GAGAACAGCT GGAAAATAGC CCATCCCGTC	120
GTTTTGGCGT GGACCCAGAT AAAGAACTTT CTTATCGCCA GCAGGCGGCC AATCTGCTTC	180
AGGACATGGG GCAGCGTCTT AACGTCTCAC AATTGACTAT CAACACTGCT ATAGTATACA	240
TGCATCGATT CTACATGATT CAGTCCTTCA CACGGTTCCC TGGAAATTCT GTGGCTCCAG	300
CAGCCTTGTT TCTAGCAGCT AAAGTGGAGG AGCAGCCCAA AAAATTGGAA CATGTCATCA	360
AGGTAGCACA TACTTGTCTC CATCCTCAGG AATCCCTTCC TGATACTAGA AGTGAGGCTT	420
ATTTGCAACA AGTTCAAGAT CTGGTCATTT TAGAAAGCAT AATTTTGCAG ACTTTAGGCT	480
TTGAACTAAC AATTGATCAC CCACATACTC ATGTAGTAAA GTGCACTCAA CTTGTTCGAG	540
CAAGCAAGGA CTTAGCACAG ACTTCTTACT TCATGGCAAC CAACAGCCTG CATTTGACCA	600
CATTTAGCCT GCAGTACACA CCTCCTGTGG TGGCCTGTGT CTGCATTCAC CTGGCTTGCA	660
AGTGGTCCAA TTGGGAGATC CCAGTCTCAA CTGACGGGAA GCACTGGTGG GAGTATGTTG	720
ACGCCACTGT GACCTTGGA CTTTTAGATG AACTGACACA TGAGTTTCTA CAGATTTTGG	780
AGAAAACCTC CAACAGGCTC AAACGCATTT GGAATTGGAG GGCATGCGAG GCTGCCAAGA	840

AAACAAAAGC AGATGACCGA GGAACAGATG AAAAGACTTC AGAGCAGACA ATCCTCAATA	900
TGATTTCCCA GAGCTCTTCA GACACAACCA TTGCAGGTTT AATGAGCATG TCAACTTCTA	960
CCACAAGTGC AGTGCCCTTCC CTGCCAGTCT CCGAAGAGTC ATCCAGCAAC TTAACCAGTG	1020
TGGAGATGTT GCCGGGCAAG CGTTGGCTGT CCTCCCAACC TTCTTTCAAA CTAGAACCTA	1080
CTCAGGGTCA TCGGACTAGT GAGAATTTAG CACTTACAGG AGTTGATCAT TCCTTACCAC	1140
AGGATGGTTC AAATGCATTT ATTTCCCAGA AGCAGAATAG TAAGAGTGTG CCATCAGCTA	1200
AAGTGTCACT GAAAGAATAC CGCGCAAGC ATGCAGAAGA ATTGGCTGCC CAGAAGAGGC	1260
AACTGGAGAA CATGGAAGCC AATGTGAAGT CACAATATGC ATATGCTGCC CAGAATCTCC	1320
TTTCTCATCA TGATAGCCAT TCTTCAGTCA TTCTAAAAAT GCCCATAGAG GGTTCAGAAA	1380
ACCCCGAGCG GCCTTTTCTG GAAAAGGCTG ACAAACAGC TCTCAAAATG AGAATCCCAG	1440
TGGCAGGTGG AGATAAAGCT GCGTCTTCAA AACCAGAGGA GATAAAAATG CGCATAAAG	1500
TCCATGCTGC AGCTGATAAG CACAATTCTG TAGAGGACAG TGTTACAAAG AGCCGAGAGC	1560
ACAAAGAAGA GCGCAAGACT CACCCATCTA ATCATCATCA TCATCATAAT CACCACTCAC	1620
ACAAGCACTC TCATTCCCAA CTTCCAGTTG GTACTGGGAA CAAACGTCCT GGTGATCCAA	1680
AACATAGTAG CCAGACAAGC AACTTAGCAC ATAAACCTA TAGCTTGTCT AGTTCTTTTT	1740
CCTCTTCCAG TTCTACTCGT AAAAGGGGAC CCTCTGAAGA GACTGGAGGG GCTGTGTTTG	1800
ATCATCCAGC CAAGATTGCC AAGAGTACTA AATCCTCTTC CCTAAATTTT TCCTTCCCTT	1860
CACTTCCTAC AATGGGTCAG ATGCCTGGGC ATAGCTCAGA CACAAGTGGC CTTTCCTTTT	1920
CACAGCCCAG CTGTAAAACT CGTGTCCCTC ATTCGAACT GGATAAAGGG CCCACTGGGG	1980
CCAATGGTCA CAACACGACC CAGACAATAG ACTATCAAGA CACTGTGAAT ATGCTTCACT	2040
CCCTGCTCAG TGCCCAGGGT GTTCAGCCCA CTCAGCCCAC TGCATTTGAA TTTGTTCGTC	2100
CTTATAGTGA CTATCTGAAT CCTCGGTCTG GTGGAATCTC CTCGAGATCT GGCAATACAG	2160
ACAAACCCCG GCCACCACCT CTGCCATCAG AACCTCCTCC ACCACTTCCA CCCCTTCCTA	2220
AGTAAAAAAA GAAAAAGAAG AGGAGAAAAA AACTTCTTTA AAAAAACACA TAATTTTTCT	2280
TTTTTTTTTTG GGGAAAAAAA AATTTTTTTT AAAATTTTTT CCCCAAGGGA CGGGGGAAAA	2340
TTTTATTTTTT AAAATTTTTT	2360

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2181 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATGGAGGGGAG AGAGGAAGAA CAACAACAAA CGGTGGTATT TCACTCGAGA ACAGCTGGAA	60
AATAGCCCAT CCCGTCGTTT TGGCGTGGAC CCAGATAAAG AACTTTCTTA TCGCCAGCAG	120
GCGGCCAATC TGCTTCAGGA CATGGGGCAG CGTCTTAACG TCTCACAATT GACTATCAAC	180
ACTGCTATAG TATACATGCA TCGATTCTAC ATGATTTCAGT CCTTCACACG GTTCCCTGGA	240
AATTCTGTGG CTCCAGCAGC CTTGTTTCTA GCAGCTAAAG TGGAGGAGCA GCCCAAAAAA	300
TTGGAACATG TCATCAAGGT AGCACATACT TGTCTCCATC CTCAGGAATC CCTTCCTGAT	360
ACTAGAAGTG AGGCTTATTT GCAACAAGTT CAAGATCTGG TCATTTTAGA AAGCATAATT	420
TTGCAGACTT TAGGCTTTGA ACTAACAATT GATCACCCAC ATACTCATGT AGTAAAGTGC	480
ACTCAACTTG TTCGAGCAAG CAAGGACTTA GCACAGACTT CTTACTTCAT GGCAACCAAC	540
AGCCTGCATT TGACCACATT TAGCCTGCAG TACACACCTC CTGTGGTGGC CTGTGTCTGC	600
ATTCACCTGG CTTGCAAGTG GTCCAATTGG GAGATCCCAG TCTCAACTGA CGGGAAGCAC	660
TGGTGGGAGT ATGTTGACGC CACTGTGACC TTGGAACTTT TAGATGAACT GACACATGAG	720
TTTCTACAGA TTTTGGAGAA AACTCCCAAC AGGCTCAAAC GCATTTGGAA TTGGAGGGCA	780
TGCGAGGCTG CCAAGAAAAC AAAAGCAGAT GACCGAGGAA CAGATGAAAA GACTTCAGAG	840
CAGACAATCC TCAATATGAT TTCCCAGAGC TCTTCAGACA CAACCATTGC AGGTTTAATG	900
AGCATGTCAA CTTCTACCAC AAGTGCAGTG CCTTCCCTGC CAGTCTCCGA AGAGTCATCC	960
AGCAACTTAA CCAGTGTGGA GATGTTGCCG GGCAAGCGTT GGCTGTCCTC CCAACCTTCT	1020
TTCAAAC TAG AACCTACTCA GGGTCATCGG ACTAGTGAGA ATTTAGCACT TACAGGAGTT	1080
GATCATTCCT TACCACAGGA TGGTTCAAAT GCATTTATTT CCCAGAAGCA GAATAGTAAG	1140
AGTGTGCCAT CAGCTAAAGT GTCAGTGAAG GAATACCGCG CGAAGCATGC AGAAGAATTG	1200
GCTGCCCAGA AGAGGCAACT GGAGAACATG GAAGCCAATG TGAAGTCACA ATATGCATAT	1260
GCTGCCCAGA ATCTCCTTTC TCATCATGAT AGCCATTCTT CAGTCATTCT AAAAATGCCC	1320
ATAGAGGGTT CAGAAAACCC CGAGCGGCCT TTTCTGGAAA AGGCTGACAA AACAGCTCTC	1380
AAAATGAGAA TCCCAGTGGC AGGTGGAGAT AAAGCTGCGT CTTCAAACC AGAGGAGATA	1440
AAAATGCGCA TAAAAGTCCA TGCTGCAGCT GATAAGCACA ATTCTGTAGA GGACAGTGTT	1500

ACAAAGAGCC GAGAGCACAA AGAAGAGCGC AAGACTCACC CATCTAATCA TCATCATCAT 1560
 CATAATCACC ACTCACACAA GCACTCTCAT TCCCAACTTC CAGTTGGTAC TGGGAACAAA 1620
 CGTCCTGGTG ATCCAAAACA TAGTAGCCAG ACAAGCAACT TAGCACATAA AACCTATAGC 1680
 TTGTCTAGTT CTTTTTCCTC TTCCAGTTCT ACTCGTAAAA GGGGACCCTC TGAAGAGACT 1740
 GGAGGGGCTG TGTTTGATCA TCCAGCCAAG ATTGCCAAGA GTACTAAATC CTCTTCCCTA 1800
 AATTTCTCCT TCCCTTCACT TCCTACAATG GGTCAGATGC CTGGGCATAG CTCAGACACA 1860
 AGTGGCCTTT CCTTTTCACA GCCCAGCTGT AAAACTCGTG TCCCTCATTC GAAACTGGAT 1920
 AAAGGGCCCA CTGGGGCCAA TGGTCACAAC ACGACCCAGA CAATAGACTA TCAAGACACT 1980
 GTGAATATGC TTCACTCCCT GCTCAGTGCC CAGGGTGTTT AGCCCACTCA GCCCACTGCA 2040
 TTTGAATTTG TTCGTCCTTA TAGTGACTAT CTGAATCCTC GGTCTGGTGG AATCTCCTCG 2100
 AGATCTGGCA ATACAGACAA ACCCCGGCCA CCACCTCTGC CATCAGAACC TCCTCCACCA 2160
 CTTCCACCCC TTCCTAAGTA A 2181

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Glu	Gly	Glu	Arg	Lys	Asn	Asn	Asn	Lys	Arg	Trp	Tyr	Phe	Thr	Arg	1	5	10	15
Glu	Gln	Leu	Glu	Asn	Ser	Pro	Ser	Arg	Arg	Phe	Gly	Val	Asp	Pro	Asp	20	25	30	
Lys	Glu	Leu	Ser	Tyr	Arg	Gln	Gln	Ala	Ala	Asn	Leu	Leu	Gln	Asp	Met	35	40	45	
Gly	Gln	Arg	Leu	Asn	Val	Ser	Gln	Leu	Thr	Ile	Asn	Thr	Ala	Ile	Val	50	55	60	
Tyr	Met	His	Arg	Phe	Tyr	Met	Ile	Gln	Ser	Phe	Thr	Arg	Phe	Pro	Gly	65	70	75	80
Asn	Ser	Val	Ala	Pro	Ala	Ala	Leu	Phe	Leu	Ala	Ala	Lys	Val	Glu	Glu	85	90	95	
Gln	Pro	Lys	Lys	Leu	Glu	His	Val	Ile	Lys	Val	Ala	His	Thr	Cys	Leu	100	105	110	
His	Pro	Gln	Glu	Ser	Leu	Pro	Asp	Thr	Arg	Ser	Glu	Ala	Tyr	Leu	Gln				

115		120		125
Gln Val Gln Asp Leu Val Ile Leu Glu Ser Ile Ile Leu Gln Thr Leu	130	135	140	
Gly Phe Glu Leu Thr Ile Asp His Pro His Thr His Val Val Lys Cys	145	150	155	160
Thr Gln Leu Val Arg Ala Ser Lys Asp Leu Ala Gln Thr Ser Tyr Phe	165	170	175	
Met Ala Thr Asn Ser Leu His Leu Thr Thr Phe Ser Leu Gln Tyr Thr	180	185	190	
Pro Pro Val Val Ala Cys Val Cys Ile His Leu Ala Cys Lys Trp Ser	195	200	205	
Asn Trp Glu Ile Pro Val Ser Thr Asp Gly Lys His Trp Trp Glu Tyr	210	215	220	
Val Asp Ala Thr Val Thr Leu Glu Leu Leu Asp Glu Leu Thr His Glu	225	230	235	240
Phe Leu Gln Ile Leu Glu Lys Thr Pro Asn Arg Leu Lys Arg Ile Trp	245	250	255	
Asn Trp Arg Ala Cys Glu Ala Ala Lys Lys Thr Lys Ala Asp Asp Arg	260	265	270	
Gly Thr Asp Glu Lys Thr Ser Glu Gln Thr Ile Leu Asn Met Ile Ser	275	280	285	
Gln Ser Ser Ser Asp Thr Thr Ile Ala Gly Leu Met Ser Met Ser Thr	290	295	300	
Ser Thr Thr Ser Ala Val Pro Ser Leu Pro Val Ser Glu Glu Ser Ser	305	310	315	320
Ser Asn Leu Thr Ser Val Glu Met Leu Pro Gly Lys Arg Trp Leu Ser	325	330	335	
Ser Gln Pro Ser Phe Lys Leu Glu Pro Thr Gln Gly His Arg Thr Ser	340	345	350	
Glu Asn Leu Ala Leu Thr Gly Val Asp His Ser Leu Pro Gln Asp Gly	355	360	365	
Ser Asn Ala Phe Ile Ser Gln Lys Gln Asn Ser Lys Ser Val Pro Ser	370	375	380	
Ala Lys Val Ser Leu Lys Glu Tyr Arg Ala Lys His Ala Glu Glu Leu	385	390	395	400
Ala Ala Gln Lys Arg Gln Leu Glu Asn Met Glu Ala Asn Val Lys Ser	405	410	415	
Gln Tyr Ala Tyr Ala Ala Gln Asn Leu Leu Ser His His Asp Ser His				

420					425					430					
Ser	Ser	Val	Ile	Leu	Lys	Met	Pro	Ile	Glu	Gly	Ser	Glu	Asn	Pro	Glu
		435					440					445			
Arg	Pro	Phe	Leu	Glu	Lys	Ala	Asp	Lys	Thr	Ala	Leu	Lys	Met	Arg	Ile
		450				455					460				
Pro	Val	Ala	Gly	Gly	Asp	Lys	Ala	Ala	Ser	Ser	Lys	Pro	Glu	Glu	Ile
		465				470					475				480
Lys	Met	Arg	Ile	Lys	Val	His	Ala	Ala	Ala	Asp	Lys	His	Asn	Ser	Val
				485							490			495	
Glu	Asp	Ser	Val	Thr	Lys	Ser	Arg	Glu	His	Lys	Glu	Glu	Arg	Lys	Thr
			500					505					510		
His	Pro	Ser	Asn	His	His	His	His	His	Asn	His	His	Ser	His	Lys	His
		515						520				525			
Ser	His	Ser	Gln	Leu	Pro	Val	Gly	Thr	Gly	Asn	Lys	Arg	Pro	Gly	Asp
		530				535					540				
Pro	Lys	His	Ser	Ser	Gln	Thr	Ser	Asn	Leu	Ala	His	Lys	Thr	Tyr	Ser
		545				550					555				560
Leu	Ser	Ser	Ser	Phe	Ser	Ser	Ser	Ser	Ser	Thr	Arg	Lys	Arg	Gly	Pro
				565							570			575	
Ser	Glu	Glu	Thr	Gly	Gly	Ala	Val	Phe	Asp	His	Pro	Ala	Lys	Ile	Ala
			580					585					590		
Lys	Ser	Thr	Lys	Ser	Ser	Ser	Leu	Asn	Phe	Ser	Phe	Pro	Ser	Leu	Pro
		595					600					605			
Thr	Met	Gly	Gln	Met	Pro	Gly	His	Ser	Ser	Asp	Thr	Ser	Gly	Leu	Ser
		610				615					620				
Phe	Ser	Gln	Pro	Ser	Cys	Lys	Thr	Arg	Val	Pro	His	Ser	Lys	Leu	Asp
		625				630					635			640	
Lys	Gly	Pro	Thr	Gly	Ala	Asn	Gly	His	Asn	Thr	Thr	Gln	Thr	Ile	Asp
				645					650					655	
Tyr	Gln	Asp	Thr	Val	Asn	Met	Leu	His	Ser	Leu	Leu	Ser	Ala	Gln	Gly
			660					665					670		
Val	Gln	Pro	Thr	Gln	Pro	Thr	Ala	Phe	Glu	Phe	Val	Arg	Pro	Tyr	Ser
			675				680					685			
Asp	Tyr	Leu	Asn	Pro	Arg	Ser	Gly	Gly	Ile	Ser	Ser	Arg	Ser	Gly	Asn
		690				695					700				
Thr	Asp	Lys	Pro	Arg	Pro	Pro	Pro	Leu	Pro	Ser	Glu	Pro	Pro	Pro	Pro
		705				710					715			720	
Leu	Pro	Pro	Leu	Pro	Lys										

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTCCCACCAA TGCTTTCC

18

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CCATCAGTTG ATACAGGGAT CT

22

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GGAATTCAGA AGGTTGTAAG ATGC

24

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACACACAGAT GTGGTGAAAT GTACCCA

27

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCATCTTACA ACCTTCTG

18

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGAATTCATG GAAAGCATTG GTGGGAAT

28

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCTCCACTAC TGGTTTGCCT GG

22

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGACTAGTAT AAATATGGCG TCGGGCCGTG

30

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
GGAGATCTTA CATGTTCAAT CCTTGGG 27

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
GGAGACAAGT ATGTGCTACC TTGATGACA 29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:
GGAATTCGGG CTGCTCCTCC ACTTTAG 27

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
GGAATTCGCT GCTGGAGCCA CAGAA 25

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:
GTGTCACTGA AAGAATACCG 20

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGAATTCAGG TGGAGATAAA GCTGC 25

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCTCTAGATA AATATGGAGG GAGAGAGGAA 30

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GGAATTCTTA CTTAGGAAGG GGTGGAAGTG 30

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGAATTCTTA CTTAGGAAGG GGTGGAAGTG GTGGAGGAGG TTAC 44

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Ala	Cys	Ser	Tyr	Ser	Pro	Thr	Ser	Pro	Ser	Tyr	Ser	Pro	Thr	Ser	Pro
1				5				10						15	
Ser	Tyr	Ser	Pro	Thr	Ser	Pro	Ser	Lys	Lys						
			20					25							